

SCORE Search Results Details for Application 10573229 and Search Result 20090528_121056_us-10-573-229a-1.rge.

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This page gives you Search Results detail for the Application 10573229 and Search Result 20090528_121056_us-10-573-229a-1.rge.

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 21:47:12 ; Search time 916 Seconds
(without alignments)
101538.085 Million cell updates/sec

Title: US-10-573-229A-1
Perfect score: 920
Sequence: 1 tctgttagagggaatggctg.....accccaaaagaaaccttcta 920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14594359 seqs, 50548307366 residues

Total number of hits satisfying chosen parameters: 29188718

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_env:
2: gb_pat:
3: gb_phg:
4: gb_pln:
5: gb_pri:
6: gb_rod:
7: gb_sts:
8: gb_syn:
9: gb_una:

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14: gb_bct:*
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16: gb_htg2:*
17: gb_htg3:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description	
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	1	920	100.0	920	2	CS074575	CS074575 Sequence
	2	920	100.0	920	2	CS430220	CS430220 Sequence
	3	920	100.0	920	2	DJ044325	DJ044325 Identific
c	4	422.2	45.9	109238	5	AL133538	AL133538 Human DNA
	5	306	33.3	308	5	Z79429	Z79429 H.sapiens f
c	6	275	29.9	140243	15	AC067760	AC067760 Homo sapi
c	7	275	29.9	147659	15	AC015496	AC015496 Homo sapi
c	8	275	29.9	172212	5	AL136100	AL136100 Human DNA
	9	226.8	24.7	186029	16	AC169795	AC169795 Macaca mu
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c	11	178.2	19.4	390	2	DJ044524	DJ044524 Identific
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	14	122.6	13.3	561	2	AR799123	AR799123 Sequence
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	16	121.2	13.2	541	2	AR612608	AR612608 Sequence
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	23	112.6	12.2	111182	5	AL359771	AL359771 Human DNA
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	26	109.6	11.9	186244	17	CU467509	CU467509 Sus scrof
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	28	108	11.7	142859	5	AC008663	AC008663 Homo sapi
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	31	105	11.4	117916	17	AC225094	AC225094 Loxodonta
	32	105	11.4	123795	17	AC218085	AC218085 Loxodonta
c	33	105	11.4	198249	16	AC165117	AC165117 Bos tauru

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ALIGNMENTS

RESULT 1

CS074575

LOCUS CS074575 920 bp DNA linear PAT 05-MAY-2005

DEFINITION Sequence 1 from Patent WO2005030250.

ACCESSION CS074575

VERSION CS074575.1 GI:63091182

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tuereci,O., Sahin,U., Helftenbein,G. and Schlueter,V.

TITLE Identification of tumour-associated cell surface antigens for diagnosis and therapy

JOURNAL Patent: WO 2005030250-A 1 07-APR-2005;
Ganymed Pharmaceuticals AG (DE)

FEATURES Location/Qualifiers

source 1..920

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 920; DB 2; Length 920;

Best Local Similarity 100.0%; Pred. No. 7.4e-275;

Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1

TCTGTAGAGGGATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60

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Qy	121	TGAGCCACTTGGAAAGCTGATCTGGAGCACCACTGCAAGCC	TTAGCTGGCTGCAGCCAC	180
Db	121	TGAGCCACTTGGAAAGCTGATCTGGAGCACCACTGCAAGCC	TTAGCTGGCTGCAGCCAC	180
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGGC	CAGAATCCCGTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGGC	CAGAATCCCGTAAATT	240
Qy	241	GCTCTTGATTCTAACCCACAGAAATTGTGAAGACCTCCAT	CAGGTGTCGACAAGGAA	300
Db	241	GCTCTTGATTCTAACCCACAGAAATTGTGAAGACCTCCAT	CAGGTGTCGACAAGGAA	300
Qy	301	GATCCCAGTAGGGCAGGAGACAGGGAGCACCTCTGCTGT	GGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCCAGTAGGGCAGGAGACAGGGAGCACCTCTGCTGT	GGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTCTGCTGGCGACTGAGAAGCATACCCACTTCCC	CAGAACCTTTTACG	420
Db	361	ATCATTGCTCTGCTGGCGACTGAGAAGCATACCCACTTCCC	CAGAACCTTTTACG	420
Qy	421	TGGAGTGAAACTTAAGGGCTGTCCAGCTAAACCTCAAAC	CTCCAGATCCATGCCAA	480
Db	421	TGGAGTGAAACTTAAGGGCTGTCCAGCTAAACCTCAAAC	CTCCAGATCCATGCCAA	480
Qy	481	TTTCTCTGCTCTGCAAAAGGACTTCAAGTGAAGACATCTG	CAGCTGTGAACGGGGTA	540
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Qy	601	GAGAGACCTCTAACCCCTGGAGAGGGAGGGAAATCTCGAG	GGACAGGGTTATGCAA	660
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Qy	661	CAACACAAGGAAGTACCTGCTGGTTCTGGGGTTGGGAAG	GGAAAATCCCTACTGCC	720
Db	661	CAACACAAGGAAGTACCTGCTGGTTCTGGGGTTGGGAAG	GGAAAATCCCTACTGCC	720
Qy	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGG	CCCCGGGGCCTGGGGGGCAC	780
Db	721	CAAGAGCCAGCCCCGAACCAAGGCACAGCTTATACTGG	CCCCGGGGCCTGGGGGGCAC	780
Qy	781	GAAAAACCTTGAAGGAGGGCGCTTCCCAGCTCCCCGGGG	TAAGGGTTACCCCCCA	840
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Qy	841 GAGGGGGGGGAAAAATCCGAGTGGATCTTCCCACCGCCGAAGACTAAAACCTTAA	900
Db	841 GAGGGGGGGGAAAAATCCGAGTGGATCTTCCCACCGCCGAAGACTAAAACCTTAA	900
Qy	901 ACCCCCCAAGAAACCTTCTA	920
Db	901 ACCCCCCAAGAAACCTTCTA	920

RESULT 2

CS430220

LOCUS CS430220 920 bp DNA linear PAT 19-OCT-2006
 DEFINITION Sequence 1 from Patent WO2006100089.
 ACCESSION CS430220
 VERSION CS430220.1 GI:116291601
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Sahin,U., Tuereci,O., Koslowski,M., Helftenbein,G., Usener,D. and
 Schlueter,V.
 TITLE Identification of surface-associated antigens for tumor diagnosis
 and therapy
 JOURNAL Patent: WO 2006100089-A 1 28-SEP-2006;
 Ganymed Pharmaceuticals AG (DE)
 FEATURES Location/Qualifiers
 source 1. .920
 /organism="Homo sapiens"
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 /db xref="taxon:9606"

ORIGIN

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Query Match      100.0%;  Score 920;  DB 2;  Length 920;
Best Local Similarity 100.0%;  Fred. No. 7.4e-275;
Matches 920;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60

Qy 61 CACTTGGTGAGAAACCGATGCCCTGCCAAACCACCTGCTGAGAC 120
Dy 61 CACTTGGTGAGAAACCGATGCCCTGCCAAACCACCTGCTGAGAC 120

Qy 121 TGAGGCCATTGGAAAGCTGATCTGGAGCACCGAGTCAGGCCCTAGCTGGCTGCAGCCAC 180
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Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGATCTGAGGCCAGAACCTGGCTAAATT	240
Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGATCTGAGGCCAGAACCTGGCTAAATT	240
Qy	241	GCTCCTGATTCTAACCCACAGAAATTGTGAAGACCTCCATCAGGTGTCGACAAGGAA	300
Db	241	GCTCCTGATTCTAACCCACAGAAATTGTGAAGACCTCCATCAGGTGTCGACAAGGAA	300
Qy	301	GATCCCAGTAGGGCAGGAGACAGGGAGCACCTCTGCTGTGCCAATGCAGGAATGCTGGCC	360
Db	301	GATCCCAGTAGGGCAGGAGACAGGGAGCACCTCTGCTGTGCCAATGCAGGAATGCTGGCC	360
Qy	361	ATCATTGCTTCTGCTGGGCAGT GAGAACGATCACCCACTTCCCCAGAACCTTTTACG	420
Db	361	ATCATTGCTTCTGCTGGGCAGT GAGAACGATCACCCACTTCCCCAGAACCTTTTACG	420
Qy	421	TGGAGTGAAAACTTAACGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCA	480
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Qy	481	TTTCTCTGCTTCTGCAAAGGACTTCAGT GAAAGACATCTGCAGCTGTGAACGGGGTA	540
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Db	601	GAGAGACCTCTAACCCCTGGAGAGGGAGGGAGGGAAATCTCGAGGACCAGGGTTATGCA	660
Qy	661	CAACACAAGGAAAGTACCTGCTGGTTCTGGGGTTGGGAAGGAAATCCCTACTGCC	720
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Qy	781	GAAAAACCTTGAAAAAGGGCGCTTCCCAGCTCCCGGGGGTAAGGGTTACCCCCCA	840
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Db 901 ACCCCCCAAGAACCTTCTA 920

RESULT 3

DJ044325

LOCUS DJ044325 920 bp DNA linear PAT 26-OCT-2007
 DEFINITION Identification of Tumour-Associated Cell Surface Antigens for Diagnosis and Therapy.
 ACCESSION DJ044325
 VERSION DJ044325.1 GI:158737401
 KEYWORDS JP 2007506417-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 920)
 AUTHORS Herufutembain,G., Shuryuta,V., Sahin,U. and Tureci,O.
 TITLE Identification of Tumour-Associated Cell Surface Antigens for Diagnosis and Therapy
 JOURNAL Patent: JP 2007506417-A 22-MAR-2007;
 Ganymed Pharmaceuticals AG
 COMMENT OS Homo sapiens
 PN JP 2007506417-A/1
 PD 22-MAR-2007
 PF 23-SEP-2004 JP 2006527354
 PR 26-SEP-2003 DE 10344799.7
 PI geert herufutembain,volker shuryuta,ugur sahin,oezlem tureci
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 FH Key Location/Qualifiers.
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ORIGIN

Query Match 100.0%; Score 920; DB 2; Length 920;
 Best Local Similarity 100.0%; Pred. No. 7.4e-275;
 Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 TCTGTAGAGGGAAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60
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 Qy 61 CACTTGGTGAGAACCGATGCCCTGCCAACCACCTGCACTAACCTGCTGGTCTGAGAC 120
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 Db 61 CACTTGGTGAGAACCGATGCCCTGCCAACCACCTGCACTAACCTGCTGGTCTGAGAC 120
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Db	181	AGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAATCCCTGGCTAAATT	240
Qy	241	GCTCTTGATTCTAACCCACAGAAATTGTGAAGACCTCCATCAGGTGTCGACAAGGAA	300
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Db	361	ATCATTGCTTCTGCTGGGCAGT GAGAACATCACCCACTTCCCCAGAACCTTTTACG	420
Qy	421	TGGAGTAAAACTTAAGGGCTGTCCAGCTAACCTCAAACCTCCAGATCCATGCCA	480
Db	421	TGGAGTAAAACTTAAGGGCTGTCCAGCTAACCTCAAACCTCCAGATCCATGCCA	480
Qy	481	TTTCTCTGCTTCTGAAAAGGACTTCAGT GAAAGACATCTG CAGCTGTGACGGGGTA	540
Db	481	TTTCTCTGCTTCTGAAAAGGACTTCAGT GAAAGACATCTG CAGCTGTGACGGGGTA	540
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Db	601	GAGAGACCTCTAACCTGGAGAGGAGGGAGGGAAATCTCGAGGACCAGGGTTATGCAA	660
Qy	661	CAACACAAGGAAAGTACCTGCTGGGTTCTGGGGTTGGGGAGGAAAATCCCTACTGCC	720
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Qy	781	GAAAACTTGAAAAGGGCGCTTCCCAGCTTCCCAGGGGGTAAGGGTTACCCCCCA	840
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Qy	841	GAGGGGGGGGGAAAAATCCGAGTGGGATCTTCCAAACGCCGAAGACTAAAACCTTAA	900
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 Db 901 ACCCCCCAAAGAACCTTCTA 920

RESULT 4
 AL133538/c

LOCUS AL133538 109238 bp DNA linear PRI 07-MAY-2008
 DEFINITION Human DNA sequence from clone RP11-550N16 on chromosome 6q26-27
 Contains a CpG island, complete sequence.
 ACCESSION AL133538
 VERSION AL133538.16 GI:12666199
 KEYWORDS HTG; CpG island.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 109238)
 AUTHORS Wallis,J.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2008) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
 Clone requests: Geneservice (<http://www.geneservice.co.uk/>) and
 BACPAC Resources (<http://bacpac.chori.org/>)
 COMMENT On Feb 5, 2001 this sequence version replaced gi:12655232.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: vega@sanger.ac.uk

 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one subclone; and the assembly was confirmed by restriction digest,
 except on the rare occasion of the clone being a YAC.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
 on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of
 human chromosome 6, constructed by the Sanger Centre Chromosome 6
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6>
 RP11-550N16 is from the library RPCI-11.2 constructed by the group

of Pieter de Jong. For further details see
<http://bacpac.chori.org/>
VECTOR: pBACe3_6.

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ORIGIN

Query Match 45.9%; Score 422.2; DB 5; Length 109238;
Best Local Similarity 94.5%; Pred. No. 3.1e-119;
Matches 460; Conservative 0; Mismatches 23; Indels 4; Gaps 2;

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 Db 95646 CACAAGG 95640

RESULT 5

Z79429

LOCUS Z79429 308 bp DNA linear PRI 23-AUG-1996

DEFINITION H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA8B6.

ACCESSION Z79429

VERSION Z79429.1 GI:1508707

KEYWORDS Anonymous marker; single read.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 308)

AUTHORS Mungall,A.J., Huckle,E., Langford,C., Ross,M.T. and Rice,C.M.

TITLE Direct Submission

JOURNAL Submitted (22-AUG-1996) The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
 humquery@sanger.ac.uk

COMMENT Vector: pBSIIISK+.

FEATURES Location/Qualifiers

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ORIGIN

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 Matches 306; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 1 ACAAGGAANATCCAGTAGGGCAGGAGACAGGAGCACCTCTGCTGTGGCCAATGCAGGAA 60

Qy 353 TGCTGGCCATCATGCTTCTGCTGGCGACTGAGAACATCACCCACTCCCCAGAACCT 412
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Qy	473	CATGCCAATTCCTGCTCTGCAAAGGACTCAAGTGAAAGACATCTGCAGCTGTGAA	532
Db	181	CATGCCAATTCCTGCTCTGCAAAGGACTCAAGTGAAAGACATCTGCAGCTGTGAA	240
Qy	533	CGGGGTAAAACCCCTCCCTGCCCCAGGCCCCAAGCAAGGATTCCTAGCGGGGAGGAAG	592
Db	241	CGGGGTAAAACCCCTCCCTGCCCCAGGCCCCAAGCAAGGATTCCTAGCGGGGAGGAAG	300
Qy	593	GTAGAATC 600	
Db	301	GTANAATC 308	

RESULT 6

AC067760/c

LOCUS AC067760 140243 bp DNA linear HTG 23-SEP-2000
DEFINITION Homo sapiens chromosome 2 clone RP11-309K2 map 2, WORKING DRAFT
SEQUENCE, 27 unordered pieces.

ACCESSION AC067760
VERSION AC067760.2 GI:10280923
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 140243)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 2, clone RP11-309K2

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 140243)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE Direct Submission
JOURNAL Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Sep 23, 2000 this sequence version replaced gi:7651809.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L9986
 Center clone name: 309_K_2
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 128933 bases at least Q40
 Consensus quality: 134958 bases at least Q30
 Consensus quality: 136879 bases at least Q20
 Insert size: 148000; agarose-fp
 Insert size: 137643; sum-of-contigs
 Quality coverage: 3.5 in Q20 bases; agarose-fp
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 27 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

*	1	4248: contig of 4248 bp in length
*	4249	4348: gap of 100 bp
*	4349	5605: contig of 1257 bp in length
*	5606	5705: gap of 100 bp
*	5706	7181: contig of 1476 bp in length
*	7182	7281: gap of 100 bp
*	7282	9012: contig of 1731 bp in length
*	9013	9112: gap of 100 bp

* 9113 10509: contig of 1397 bp in length
 * 10510 10609: gap of 100 bp
 * 10610 13120: contig of 2511 bp in length
 * 13121 13220: gap of 100 bp
 * 13221 15323: contig of 2103 bp in length
 * 15324 15423: gap of 100 bp
 * 15424 17407: contig of 1984 bp in length
 * 17408 17507: gap of 100 bp
 * 17508 20878: contig of 3371 bp in length
 * 20879 20978: gap of 100 bp
 * 20979 22666: contig of 1688 bp in length
 * 22667 22766: gap of 100 bp
 * 22767 26227: contig of 3461 bp in length
 * 26228 26327: gap of 100 bp
 * 26328 29552: contig of 3225 bp in length
 * 29553 29652: gap of 100 bp
 * 29653 33144: contig of 3492 bp in length
 * 33145 33244: gap of 100 bp
 * 33245 35959: contig of 2715 bp in length
 * 35960 36059: gap of 100 bp
 * 36060 40873: contig of 4814 bp in length
 * 40874 40973: gap of 100 bp
 * 40974 46108: contig of 5135 bp in length
 * 46109 46208: gap of 100 bp
 * 46209 50453: contig of 4245 bp in length
 * 50454 50553: gap of 100 bp
 * 50554 54780: contig of 4227 bp in length
 * 54781 54880: gap of 100 bp
 * 54881 60935: contig of 6055 bp in length
 * 60936 61035: gap of 100 bp
 * 61036 68604: contig of 7569 bp in length
 * 68605 68704: gap of 100 bp
 * 68705 75243: contig of 6539 bp in length
 * 75244 75343: gap of 100 bp
 * 75344 81214: contig of 5871 bp in length
 * 81215 81314: gap of 100 bp
 * 81315 87663: contig of 6349 bp in length
 * 87664 87763: gap of 100 bp
 * 87764 94389: contig of 6626 bp in length
 * 94390 94489: gap of 100 bp
 * 94490 105834: contig of 11345 bp in length
 * 105835 105934: gap of 100 bp
 * 105935 125401: contig of 19467 bp in length
 * 125402 125501: gap of 100 bp
 * 125502 140243: contig of 14742 bp in length.

FEATURES

source

Location/Qualifiers

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/map="2"
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/clone_lib="RPCI-11 Human Male BAC"
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/note="assembly_fragment;
clone_end:SP6;
vector_side:left"
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              /note="assembly_fragment"
/gap           35960. .36059
              /estimated_length=100
/misc_feature 36060. .40873
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              /estimated_length=100
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Query Match 29.9%; Score 275; DB 15; Length 140243;
 Best Local Similarity 100.0%; Pred. No. 2.7e-73;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCTGTAGAGGGAAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	60
Db	51788	TCTGTAGAGGGAAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG	51729
Qy	61	CACTTGGTGAGAAAACCGATGCCCTGCAACCACCTGCAC	120
Db	51728	CACTTGGTGAGAAAACCGATGCCCTGCAACCACCTGCAC	51669
Qy	121	TGAGCCACTTGGAAAGCTGATCTGGAGCACCAAGTCAAGCCCTAGCTGGCTGCAGCCAC	180
Db	51668	TGAGCCACTTGGAAAGCTGATCTGGAGCACCAAGTCAAGCCCTAGCTGGCTGCAGCCAC	51609
Qy	181	AGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAATCCCTGGCTAAATT	240
Db	51608	AGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAATCCCTGGCTAAATT	51549
Qy	241	GCTCCTTGATTCTAACCCACAGAAATTGTGTAAG	275
Db	51548	GCTCCTTGATTCTAACCCACAGAAATTGTGTAAG	51514

RESULT 7
 AC015496/c

LOCUS AC015496 147659 bp DNA linear HTG 16-MAR-2000
 DEFINITION Homo sapiens clone RP11-21E5, WORKING DRAFT SEQUENCE, 7 unordered pieces.
 ACCESSION AC015496

VERSION AC015496.3 **GI:**7249030
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 147659)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-21E5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 147659)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 16, 2000 this sequence version replaced gi:6553986.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3993
Center clone name: 21_E_5
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 129300 bases at least Q40
Consensus quality: 140951 bases at least Q30
Consensus quality: 145175 bases at least Q20
Insert size: 146000; agarose-fp
Insert size: 147059; sum-of-contigs

Quality coverage: 5.8 in Q20 bases; agarose-fp
 Quality coverage: 5.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

- * 1 2851: contig of 2851 bp in length
- * 2852 2951: gap of 100 bp
- * 2952 6911: contig of 3960 bp in length
- * 6912 7011: gap of 100 bp
- * 7012 13475: contig of 6464 bp in length
- * 13476 13575: gap of 100 bp
- * 13576 29402: contig of 15827 bp in length
- * 29403 29502: gap of 100 bp
- * 29503 54805: contig of 25303 bp in length
- * 54806 54905: gap of 100 bp
- * 54906 87698: contig of 32793 bp in length
- * 87699 87798: gap of 100 bp
- * 87799 147659: contig of 59861 bp in length.

FEATURES

	Location/Qualifiers
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misc_feature	7012. .13475 /note="assembly_fragment"
gap	13476. .13575 /estimated_length=100
misc_feature	13576. .29402 /note="assembly_fragment"
gap	29403. .29502 /estimated_length=100
misc_feature	29503. .54805 /note="assembly_fragment"

gap 54806. .54905
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 clone_end:SP6;
 vector_side:right"

ORIGIN

Query Match 29.9%; Score 275; DB 15; Length 147659;
 Best Local Similarity 100.0%; Pred. No. 2.8e-73;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60
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 Db 411178 TCTGTAGAGGGGAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 41119

Qy 61 CACTGGTGAGAAACCGATGCCCTGCCAACCACCTGCACTAACCTGCTGGTCTGAGAC 120
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 Db 41118 CACTGGTGAGAAACCGATGCCCTGCCAACCACCTGCACTAACCTGCTGGTCTGAGAC 41059

Qy 121 TGAGCCACTTGGAGCTGATCTGGAGCACCACTGCAAGCCCTAGCTGGCTGCAGCCAC 180
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 Db 41058 TGAGCCACTTGGAGCTGATCTGGAGCACCACTGCAAGCCCTAGCTGGCTGCAGCCAC 40999

Qy 181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCTGGCTAAATT 240
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 Db 40998 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCTGGCTAAATT 40939

Qy 241 GCTCCTTGATTCTAACCCACAGAAATTGTGTAAG 275
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 Db 40938 GCTCCTTGATTCTAACCCACAGAAATTGTGTAAG 40904

RESULT 8

AL136100/c

LOCUS AL136100 172212 bp DNA linear PRI 06-MAY-2008
 DEFINITION Human DNA sequence from clone RP11-534P19 on chromosome 6 Contains a pseudogene similar to zinc finger proteins, complete sequence.
 ACCESSION AL136100
 VERSION AL136100.12 GI:11322762
 KEYWORDS HTG; zinc finger.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 172212)

AUTHORS Bird,C.

TITLE Direct Submission

JOURNAL Submitted (30-APR-2008) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk

Clone requests: Geneservice (<http://www.geneservice.co.uk/>) and BACPAC Resources (<http://bacpac.chori.org/>)

COMMENT On Nov 23, 2000 this sequence version replaced gi:11139882.

Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>
RP11-534P19 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://bacpac.chori.org/>
VECTOR: pBACe3.6.

FEATURES Location/Qualifiers

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/db_xref="taxon:9606"
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/clone="RP11-534P19"
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misc_feature 101..172212
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gene complement(26702..26930)
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CDS complement(26702..26930)
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Tr:Q96DL8 Tr:Q9P220"

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ORIGIN

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Query Match          29.9%; Score 275; DB 5; Length 172212;
Best Local Similarity 100.0%; Pred. No. 2.8e-73;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCTGTAGAGGGAAATGGCTGCTGTATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60
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Db     93324 TCTGTAGAGGGAAATGGCTGCTGTATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 93265

Qy      61 CACTTGGTGAGAAAACCAGTCCTCTGCCAACCAACCTGCACAACTGCTGGGCTGAGAC 120
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Db     93264 CACTTGGTGAGAAAACCAGTCCTCTGCCAACCAACCTGCACAACTGCTGGGCTGAGAC 93205

Qy      121 TGAGCCACTTGGAAAGCTGATCTGGAGCACCAAGTCAGGCCCTAGCTGGCTGCAGCCAC 180
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Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGGCCAGAATCCCTGGCTAAATT 240
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Db     93144 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGGCCAGAATCCCTGGCTAAATT 93085

Qy      241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 275
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Db     93084 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAG 93050

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RESULT 9

AC169795

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LOCUS      AC169795           186029 bp    DNA    linear   HTG 12-NOV-2005
DEFINITION Macaca mulatta clone CH250-283M17, WORKING DRAFT SEQUENCE, 3
ordered pieces.
ACCESSION  AC169795
VERSION    AC169795.2 GI:82174563
KEYWORDS   HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE     Macaca mulatta (rhesus monkey)
ORGANISM   Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE  1 (bases 1 to 186029)
AUTHORS   Muzny,D.M., Abraham,K.K., Abulimiti,A., Adams,C.Q., Aduba,G.,
          Allen,C.C., Alsbrooks,S.L., Anosike,U.S., Archer,P.M.,
          Arredondo,H.H., Attaway,T., Bandaranaike,D.P., Bangura,L.,
          Barton,S.R., Bell,A.V., Bell,S.N., Beraducci,A.R., Bickham,C.,
          Biswalo,K., Blyth,P.R., Buhay,C.J., Canada,A., Cardenas,V.,

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Carter,K., Chacko,J., Chandrabose,M.N., Chavez,A., Chavez,D., Chen,G., Chen,R., Chu,H., Clerc blankenburg,K.P., Cockrell,R., Cooper,J.A., Coyle,M.D., Cree,A., Cueto,C.B., Curry,S.M., Dai,W., Dao,M.D., Davila,M., Davis,C., Davy-Carroll,L., Del fierro,P., Demen,R., Denson,S., Ding,Y., Dinh,H.H., Donlin,J.E., Dugan-Rocha,S., Dunn,A.M., Durbin,K.J., Ebong,V.E., Egan,A., Espinosa,V.C., Fa,M., Fernandez,S., Fernando,P.R., Ferrer,A.R., Flagg,N., Forbes,L.D., Fowler,R.G., Fu,Q., Fuh,E., Gabisi,R.A., Ganardhanan,M., Ganer,J., Garcia iii,R.M., Garcia,A.M., Garcia,S.M., Garner,T.T., Ghose,S., Gingras,M., Gonzalez-Garay,M.L., Guevara,W.V., Haaland,W.C., Haeberlen,K.A., Hagans,B.J., Hall,O., Hamid,H., Hamilton,K.A., Hampton,O.A., Harbes,B.A., Harris,R.A., Havlak,P., Hawes,A.C., Hawkins,E.S., Haynes,S.J., Hemphill,L., Hernandez,J., Hines,S., Hirani,K., Hitchens,M.E., Hodgson,A.V., Hogues,M.E., Holder,M., Hollins,B., Howell,L.L., Hulyk,S.W., Hume,J., Jackson,A., Jackson,L.R., Jacob,S.K., Jhangiani,S.N., Jiang,H., Johnson,B., Johnson,R., Joshi,V., Joy,C., Kaikai,F.B., Kalafus,K.J., Kalu,J.B., Kang,Y., Keebler,J., Khan,Z.M., Kidwai,S., King,L.M., Kisamo,H., Kovar,C.L., Kowis,A.N., Kowis,C.R., Lago,L.A., Lago,M.T., Lai,C., Lara,F., Le,T.T., Lee,S.L., Lee,T.W., Legall iii,F.H., Lemon,S.J., Lewis,L.R., Li,B., Li,Y., Li,Z., Linnell,M.A., Liu,J., Liu,W., Liu,Y., Liu,Y., Liyanage,D., London,P., Lopez,J., Lorenshuwela,L.M., Lozado,R.J., Luc,T., Madu,R.C., Maheshwari,M., Maheshwari,R., Malloy,K., Mansouri,D.L., Martinez,E., Matejkova,P., Mathew,T., Mccauley,S.K., Mcpherson,J.D., Mercado,C., Mercado,I.C., Metzker,M.L., Millin,A., Milosavljevic,A., Morgan,M.B., Morris,S., Munidas,M., Murray,D.D., Muzny,D.M., Nazareth,L.V., Ngo,D.N., Nguyen,H.T., Nguyen,N.B., Nguyen,P.Q., Nwaokelemech,O.O., Obregon,M., Odeh,E.A., Okonkwo,F., Okwuonu,G.O., Okwuonu,K.C., Onyenekwe,J., Parish,B.J., Parker,D.N., Parra,A.A., Pasternak,S., Patel,B.M., Patel,R.R., Paul,H.A., Perez,A., Perez,L.M., Perez,Y.Y., Pham,T.L., Player,E.J., Primus,E.L., Pu,L., Puazo,M., Purkiss,C., Qin,X., Quiroz,J.B., Rabata,D., Rachlin,E.K., Ren,Y., Richards,S., Rojas,A., Ruiz,S., Sabo,A., Santibanez,J., Savery,G.G., Scherer,S.E., Schneider,B.W., Sebasigari,R., Sexton,M.M., Shen,H., Shen,Y., Sisson,I., Sneed,A.J., Sodergren,E., Song,X., Sorelle,R.P., Svatek,A.F., Taylor,E.W., Taylor,T.R., Thelus,R., Thomas,N., Thorn,R.D., Thornton,R.D., Tong,M.Y., Trejos,Z.Y., Usmani,K., Vargo,C.E., Vattathil,S., Vega,R.A., Villasana,D., Volkov,A., Walker,D.L., Wang,Q., Wang,S., Warren,J.T., Watt,J.E., Wei,X., Wheeler,D.A., White,C.S., Williams jr,R.L., Williams,A.C., Williams,G.A., Williams,J.D., Wilson,K., Woodworth,J.R., Worley,K.C., Wright,R.A., Wu,J., Wu,W., Yakub,S., Yerrapragada,S., Yu,F., Yuan,D.T., Yuan,Y., Zhang,J., Zhang,L., Zhang,Z., Zhou,J., Zhu,Y., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 186029)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (12-OCT-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 186029)

AUTHORS Worley, K.C.

TITLE Direct Submission

JOURNAL Submitted (12-NOV-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 12, 2005 this sequence version replaced gi:77539482.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help.tmc.edu

----- Project Information

Center project name: LDVL

Center clone name: CH250-283M17

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 186011 bases at least Q40

Consensus quality: 186345 bases at least Q30

Consensus quality: 186634 bases at least Q20

Estimated insert size: 205029; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 * The sequence data in this record represents an 'enhanced' version
 * of a Phase 2 submission. The indicated order and orientation of
 * each sequence has been established using one or more of the
 * following: read-pair data from individual subclones, overlaps
 * with neighboring clones, alignment with available reference
 * sequence (e.g., human), and/or confirmation by PCR testing.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 54276: contig of 54276 bp in length
 * 54277 54376: gap of 100 bp
 * 54377 104140: contig of 49764 bp in length
 * 104141 104340: gap of 200 bp
 * 104341 186029: contig of 81689 bp in length.

FEATURES Location/Qualifiers

source 1. .186029
 /organism="Macaca mulatta"
 /mol_type="genomic DNA"
 /db_xref="taxon:9544"
 /clone="CH250-283M17"

misc_feature 1. .54276
 /note="assembly_name:Contig35"

misc_feature 54277. .54376
 /note="assembly_name:gap"

gap 54277. .54376
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misc_feature 54377. .104140
 /note="assembly_name:Contig39"

misc_feature 104141. .104340
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gap 104141. .104340
 /estimated_length=200

misc_feature 104341. .186029
 /note="assembly_name:Contig40"

ORIGIN

Query Match 24.7%; Score 226.8; DB 16; Length 186029;
 Best Local Similarity 91.3%; Fred. No. 3.1e-58;
 Matches 252; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

Qy 1 TCTGTAGAGGGAAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTG 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 152352 TCTATAGAGGAGAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCCGGTGGAGAGGTG 152411

Qy 61 CACTTGGTGAGAAAACCGATGCCCTGCAACCACCTGCACTAACCTGCTGGTCTGAGAC 120
 ||||| ||||| | ||| ||||| ||||| | ||||| ||||| | ||||| ||||| |||||
 Db 152412 CACTTGGTGAGAAAACATGCCCTGCAACCACCTACGCTAACCTGCTAGGCCTGAGAC 152471

Qy 121 TGAGCCACTTGGAGCTGATCTGGAGCACCA--GTCAAGCCCTAGCTGGCTGCAGCC 178
 ||||| ||||| ||||| ||||| ||||| | ||||| ||||| ||||| |||||
 Db 152472 TGAGCCACTTGGAGCTGATCTGGAGCACTAAGTCAGCCTCAGCTGACTGCAGCC 152531

Qy 179 ACAGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAATCCCTGGCTAAA 238
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 152532 CCAGCCAACAATAAGACTGCAACCTCCTGGGAATCCTGAGCCAGAATCCCTGGCTAAA 152591

Qy 239 TTGCTCCTTGATTCTTAACCCACAGAAAATTGTGTAA 274
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 152592 TTGATCCTTCATTCTTAACCCACCGAAAATTGTGTGA 152627

RESULT 10
 CS074841/c

LOCUS CS074841 390 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 267 from Patent WO2005030250.

ACCESSION CS074841
 VERSION CS074841.1 GI:63091381
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Tuereci,O., Sahin,U., Helftenbein,G. and Schlueter,V.
 TITLE Identification of tumour-associated cell surface antigens for
 diagnosis and therapy
 JOURNAL Patent: WO 2005030250-A 267 07-APR-2005;
 Ganymed Pharmaceuticals AG (DE)
 FEATURES Location/Qualifiers
 source 1. .390
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 19.4%; Score 178.2; DB 2; Length 390;
 Best Local Similarity 93.5%; Fred. No. 2e-43;
 Matches 186; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy	328	ACCTCTGCTGTGCCAATGCAGGAATGCTGGCCATCATTGCTTCTGCTGGCGACTGAGA	387
Db	264	ATCTCTGCTGTGCCAATGCAGGAATGCTGGCCATCATTGCTTCTGCTGGCGACTGAGA	205
Qy	388	AGCATCACCCACTTCCCCAGAACCTTTTACGTGGAGTGAAACCTTAAGGGCTGTCC	447
Db	204	AGCATCACCCACTTCCCCAGAACCTTTTACGTGGAGTGAAACCTTAAGGGCTGTCC	145
Qy	448	AGCTAACCTCCAACCTCCAGATCCCAGATGCCAATTCTCTGCTTCTGCAAAAGGACTCA	507
Db	144	AGCTAACCTCCAACCTCCAGATCCCAGATGCCAATTCTCTGCTTCTGCAAAAGGACTCAT	85
Qy	508	AGTGAAAGACATCTGCAGC	526
Db	84	GGCGAGCGTTATCCACAGC	66

RESULT 11
 DJ044524/c

LOCUS	DJ044524	390 bp	DNA	linear	PAT 26-OCT-2007
DEFINITION	Identification of Tumour-Associated Cell Surface Antigens for Diagnosis and Therapy.				
ACCESSION	DJ044524				
VERSION	DJ044524.1 GI:158738196				
KEYWORDS	JP 2007506417-A/200.				

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 390)
AUTHORS Herufutembain,G., Shuryuta,V., Sahin,U. and Tureci,O.
TITLE Identification of Tumour-Associated Cell Surface Antigens for
Diagnosis and Therapy
JOURNAL Patent: JP 2007506417-A 200 22-MAR-2007;
Ganymed Pharmaceuticals AG
COMMENT OS Homo sapiens
PN JP 2007506417-A/200
PD 22-MAR-2007
PF 23-SEP-2004 JP 2006527354
PR 26-SEP-2003 DE 10344799.7
PI geert herufutembain,volker shuryuta,ugur sahin,oezlem tureci
CC
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .390
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 19.4%; Score 178.2; DB 2; Length 390;
Best Local Similarity 93.5%; Pred. No. 2e-43;
Matches 186; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 328 ACCTCTGCTGTGGCCAATGCAGGAATGCTGGCCATCATTCCTCTGCTGGCGACTGAGA 387
Db 264 ATCTCTGCTGTGGCCAATGCAGGAATGCTGGCCATCATTCCTCTGCTGGCGACTGAGA 205
Qy 388 AGCATCACCCACTTCCCCAGAACCTTTACGTGGAGTGAAACTTAAGGGCTGTCC 447
Db 204 AGCATCACCCACTTCCCCAGAACCTTTACGTGGAGTGAAACTTAAGGGCTGTCC 145
Qy 448 AGCTAAACCTCCAACCTCCAGATCCCATTCTCTGCTCTGCAAAAGGACTTCA 507
Db 144 AGCTAAACCTCCAACCTCCAGATCCCATTCTCTGCTCTGCAAAAGGACTCAT 85
Qy 508 AGTGAAGAGACATCTGCAGC 526
Db 84 GGGCAGCGTTATCCACAGC 66

RESULT 12
CS430486/G

LOCUS CS430486 390 bp DNA linear PAT 19-OCT-2006
DEFINITION Sequence 267 from Patent WO2006100089

ACCESSION CS430486
 VERSION CS430486.1 GI:116291800
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Sahin,U., Tuereci,O., Koslowski,M., Helftenbein,G., Usener,D. and
 Schlueter,V.
 TITLE Identification of surface-associated antigens for tumor diagnosis
 and therapy
 JOURNAL Patent: WO 2006100089-A 267 28-SEP-2006;
 Ganymed Pharmaceuticals AG (DE)
 FEATURES Location/Qualifiers
 source 1..390
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 19.2%; Score 176.6; DB 2; Length 390;
 Best Local Similarity 93.0%; Pred. No. 6.3e-43;
 Matches 185; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 328 ACCTCTGCTGTGCCAATGCAGGAATGCTGCCATATTGCTCTGCTGGCGACTGAGA 387
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 Db 264 ATCTCTGCTGTGCCAATGCAGGAATGCTGCCATATTGCTCTGCTGGCGACTGAGA 205
 Qy 388 AGCATCACCCACTTCCCAGAACCTTTTACGTGGAGTGAAAACTTAACGGGCTGTCC 447
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 Db 204 AGCATCACCCACTTCCCAGAACCTTTTACGTGGAGTGAAAACTTAACGGGCTGTCC 145
 Qy 448 AGCTAACCTCCAACCTCCAGATCCCATGCCAATTCTGCTCTGCAAAGGACTTCA 507
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 Db 144 AGCTAACCTCCAACCTCCAGATWCCATGCCAATTCTGCTCTGCAAAGGACTCAT 85
 Qy 508 AGTGAAGACATCTGCAGC 526
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 Db 84 GGGCAGCGTTATCCACAGC 66

RESULT 13

AR612609

LOCUS AR612609 561 bp DNA linear PAT 15-DEC-2004
 DEFINITION Sequence 108 from patent US 6828097.
 ACCESSION AR612609
 VERSION AR612609.1 GI:56668431
 KEYWORDS .

SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 561)
 AUTHORS Knoll, J.H.M. and Rogan, P.K.
 TITLE Single copy genomic hybridization probes and method of generating same
 JOURNAL Patent: US 6828097-A 108 07-DEC-2004;
 The Childrens Mercy Hospital; Kansas City, MO
 FEATURES Location/Qualifiers
 source 1..561
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 13.3%; Score 122.6; DB 2; Length 561;
 Best Local Similarity 69.6%; Fred. No. 4.7e-26;
 Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
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 Db 201 CTCTGGGGAAAGCCAGCTGCCATGTGATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC 260

Qy 62 ACTTGGTGAGAACCGATGCCT-CTGCCAACACCACCTGCACTAACCTGCTGGTC----- 114
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 261 ATGTGGCAAGGAACGTGAGGCCCTCTGCCAACAGCCAGCAAGGAACGTGAGGCCCTGCCA 320

Qy 115 -----TGAGACTGAGCCACTTGGAAAGCTGATCTGGAGCACAGTCAGGCCCTTAGC 167
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 321 ACAGCCATGTGAGTGAGCCATCTGGAAAGCAGATCCTCCAGCCCCAGTCAGCCTCAGA 380

Qy 168 TGGCTGCAGCCACAGCCAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAAC 227
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 381 TGAATGCAGCCCCAGCTAACATCTGACTGCAACCTCATGAGAGACCCCTGAGCCAGAAC 440

Qy 228 CCCTGGCTAAATTGCTCCTGATTCTAACCCACAGAAATTGTGTAAGA 276
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 441 ACCCAGCTAAGCTGCTCTAACATTCTGACCCACAGAAACTGTGAGAGA 489

RESULT 14

AR799123

LOCUS AR799123 561 bp DNA linear PAT 05-APR-2006
 DEFINITION Sequence 108 from patent US 7014997.
 ACCESSION AR799123
 VERSION AR799123.1 GI:91151193
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 561)

AUTHORS Knoll, J.H.M. and Rogan, P.K.
 TITLE Chromosome structural abnormality localization with single copy probes
 JOURNAL Patent: US 7014997-A 108 21-MAR-2006;
 The Children's Mercy Hospital; Kansas City, MO;
 US;
 FEATURES Location/Qualifiers
 source 1. .561
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 13.3%; Score 122.6; DB 2; Length 561;
 Best Local Similarity 69.6%; Fred. No. 4.7e-26;
 Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;
 Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
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 Db 201 CTCTGGGGAAGCCAGCTGCCATGTGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC 260
 Qy 62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACCTGCACTAACCTGCTGGTC----- 114
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 261 ATGTGGCAAGGAACTGAGGCCTCCTGCCAACAGCCAGCAAGGAACTGAGGCCTCCTGCCA 320
 Qy 115 -----TGAGACTGAGCCACTTGGAGCTGATCTGGAGCACAGTCAGCCCTTAGC 167
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 321 ACAGCCATGTGAGTGAGCCATCTTGGAGCAGATCTCCAGCCCCAGTCAGCCTTCAGA 380
 Qy 168 TGGCTGCAGCCACAGCCAACACAAGACTGCAACCTCCTGGGGATCTGAGCCAGAAC 227
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 Db 381 TGAUTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAAC 440
 Qy 228 CCCTGGCTAAATTGCTCCTGATTCTAACCCACAGAAATTGTGTAAGA 276
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 Db 441 ACCCAGCTAACAGCTGCCCTAACATTCTGACCCACAGAAACTGTGAGAGA 489

RESULT 15

DD052947

LOCUS DD052947 561 bp DNA linear PAT 04-NOV-2005
 DEFINITION SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME.
 ACCESSION DD052947
 VERSION DD052947.1 GI:92688538
 KEYWORDS JP 2004523201-A/108.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 561)

AUTHORS Joan,K.H.M., Rogan,P.K. and Kazarro,P.M.

TITLE SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

JOURNAL Patent: JP 2004523201-A 108 05-AUG-2004;
KNOLL H JOAN,PETER K ROGAN

COMMENT OS Homo sapiens
PN JP 2004523201-A/108
PD 05-AUG-2004
PF 15-MAY-2001 JP 2001585298
PR 16-MAY-2000 US 09/573080,14-MAY-2001 US 09/854867 PI
knoll h m joan,peter k rogan,patricia m kazarro CC
FH Key Location/Qualifiers
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FT misc_feature (62)..(62)
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FT /note='n is a, c, g or t'.
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/organism="Homo sapiens"
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ORIGIN

Query Match 13.3%; Score 122.6; DB 2; Length 561;
Best Local Similarity 69.6%; Pred. No. 4.7e-26;
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy	2 CTGTAGGGGAATGGCTGCTGTATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC	61
Db	201 CTCTGGGGAAGCCAGCTGCCATGTATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC	260
Qy	62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACCTGCACTAACCTGCTGGTC-----	114
Db	261 ATGTGGCAAGGAACTGAGGCCTCCTGCCAACAGCCAGCAAGGAAGTGGCCTCCTGCCA	320
Qy	115 -----TGAGACTGAGCCACTTGGAGCTGATCTGGAGCACAGTCAGCCCTTAGC	167
Db	321 ACAGCCATGTGAGTGAGCCATCTGGAGCAGATCCTCAGCCCCAGTCAGCCTTCAGA	380
Qy	168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAAC	227
Db	381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAAC	440
Qy	228 CCCGGCTAAATTGCTCCTGATTCTAACCCACAGAAATTGTGTAAGA	276
Db	441 ACCCAGCTAACAGCTGCTCCTAACATTCTGACCCACAGAAACTGTGAGAGA	489

Search completed: May 31, 2009, 22:03:09

Job time : 957 secs

SCORE 3.0